



IFWO

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/804,762

DATE: 07/27/2004

TIME: 12:46:57

Input Set : A:\A-72186.ST25.txt

Output Set: N:\CRF4\07272004\J804762.raw

3 <110> APPLICANT: Qi, Yan  
 4 Zhang, Xianghua  
 5 Konigsberg, Paula  
 7 <120> TITLE OF INVENTION: Specific Inhibition of Allorejection  
 9 <130> FILE REFERENCE: A-72186/TAL/DCF (471702-00005)  
 11 <140> CURRENT APPLICATION NUMBER: US 10/804,762  
 12 <141> CURRENT FILING DATE: 2004-03-19  
 14 <150> PRIOR APPLICATION NUMBER: US 60/456,378  
 15 <151> PRIOR FILING DATE: 2003-03-19  
 17 <160> NUMBER OF SEQ ID NOS: 32  
 19 <170> SOFTWARE: PatentIn version 3.2  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 235  
 23 <212> TYPE: PRT  
 24 <213> ORGANISM: Homo sapiens  
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 29 1 5 10 15  
 32 His Ala Ala Arg Pro Ser Gln Phe Arg Val Ser Pro Leu Asp Arg Thr  
 33 20 25 30  
 36 Trp Asn Leu Gly Glu Thr Val Glu Leu Lys Cys Gln Val Leu Leu Ser  
 37 35 40 45  
 40 Asn Pro Thr Ser Gly Cys Ser Trp Leu Phe Gln Pro Arg Gly Ala Ala  
 41 50 55 60  
 44 Ala Ser Pro Thr Phe Leu Leu Tyr Leu Ser Gln Asn Lys Pro Lys Ala  
 45 65 70 75 80  
 48 Ala Glu Gly Leu Asp Thr Gln Arg Phe Ser Gly Lys Arg Leu Gly Asp  
 49 85 90 95  
 52 Thr Phe Val Leu Thr Leu Ser Asp Phe Arg Arg Glu Asn Glu Gly Tyr  
 53 100 105 110  
 56 Tyr Phe Cys Ser Ala Leu Ser Asn Ser Ile Met Tyr Phe Ser His Phe  
 57 115 120 125  
 60 Val Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg  
 61 130 135 140  
 64 Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg  
 65 145 150 155 160  
 68 Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly  
 69 165 170 175  
 72 Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr  
 73 180 185 190  
 76 Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His  
 77 195 200 205  
 80 Arg Asn Arg Arg Arg Val Cys Lys Cys Pro Arg Pro Val Val Lys Ser

**ENTERED**

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85 225      230      235
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90 <212> TYPE: DNA
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98 tggccttacc agtgaccgcc ttgctcctgc cgctggcctt gctgctccac gccgccaggc      180
100 cgagccagtt ccgggtgtcg ccgctggatc ggacctggaa cctgggcgag acagtggagc      240
102 tgaagtgccg ggtgctgctg tccaaccgca cgtcgggctg ctgctggctc tccagccgc      300
104 gcggcgccgc cgccagtcct accttccctc tatacctctc ccaaaacaag cccaaggcgg      360
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110 ccatcatgta cttcagccac ttcgtgcggg tcttctgccg agcgaagccc accacgacgc      540
112 cagcgccgcg accaccaaca ccggcgccca ccatcgcgtc gcagcccctg tccctgcgcc      600
114 cagaggcgct ccggccagcg gcggggggcg cagtgcacac gagggggctg gacttcgcct      660
116 gtgatatacta catctgggcg cccttgggcg ggacttggtg ggtccttctc ctgtcactgg      720
118 ttatcaccct ttactgcaac cacaggaacc gaagacgtgt ttgcaaagt ccccggcctg      780
120 tgggtcaaata gggagacaag ccagcccttt cggcgagata cgtctaacc tgtgcaacag      840
122 ccactacatt acttcaaaact gagatccttc cttttgaggg agcaagtcct tccctttcat      900
124 tttttccagt cttcctccct gtgtattcat tctcatgatt attatttttag tgggggcggg      960
126 gtgggaaaga ttactttttt tttatgtgtt tgacgggaaa caaaactagg taaaatctac      1020
128 agtacaccac aagggtcaca atactgttgt gcgcacatcg cggtagggcg tggaaagggg      1080
130 caggccagag ctaccgcgag agttctcaga atcatgctga gagagctgga ggcacccatg      1140
132 ccatctcaac ctcttccccc cccgttttac aaagggggag gctaaagccc agagacagct      1200
134 tgatcaaagg cacacagcaa gtcagggttg gagcagtagc tggagggacc ttgtctccca      1260
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142 aatgtaaaaa atatcagact tttttttttt ataataaagc ctaaaattgt atagacctaa      1500
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146 ctctgtgaaa cccctatgtg gaggcggaat tgctctccca gcccttgcat tgcagagggg      1620
148 cccatgaaag aggacaggct acccctttac aaatagaatt tgagcatcag tgagggtaaa      1680
150 ctaaggccct cttgaatctc tgaatttgag atacaaacat gttcctggga tcaactgatga      1740
152 cttttttatac tttgtaaaaga caattgttgg agagccctc acacagccct ggctctgct      1800
154 caactagcag atacaggat gaggcagacc tgactctctt aaggaggctg agagcccaaa      1860
156 ctgctgtccc aaacatgcac ttccttgctt aagggtatgtt acaagcaatg cctgccatt      1920
158 ggagagaaaa aacttaagta gataaggaaa taagaaccac tcataattct tcaccttagg      1980
160 aataatctcc tgtaaatatg gtgtacattc ttctgatta ttttctacac atacatgtaa      2040
162 aatatgtctt tcttttttaa atagggttgt actatgctgt tatgagtggc tttaatgaat      2100
164 aacattttgt agcatcctct ttaatgggta aacagcaaaa aaaaaaaaaa aaaaaaaaaa      2160
166 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      2220
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171 <210> SEQ ID NO: 3
172 <211> LENGTH: 198
173 <212> TYPE: PRT

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Output Set: N:\CRF4\07272004\J804762.raw

174 <213> ORGANISM: Homo sapiens  
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 179 1 5 10 15  
 182 His Ala Ala Arg Pro Ser Gln Phe Arg Val Ser Pro Leu Asp Arg Thr  
 183 20 25 30  
 186 Trp Asn Leu Gly Glu Thr Val Glu Leu Lys Cys Gln Val Leu Leu Ser  
 187 35 40 45  
 190 Asn Pro Thr Ser Gly Cys Ser Trp Leu Phe Gln Pro Arg Gly Ala Ala  
 191 50 55 60  
 194 Ala Ser Pro Thr Phe Leu Leu Tyr Leu Ser Gln Asn Lys Pro Lys Ala  
 195 65 70 75 80  
 198 Ala Glu Gly Leu Asp Thr Gln Arg Phe Ser Gly Lys Arg Leu Gly Asp  
 199 85 90 95  
 202 Thr Phe Val Leu Thr Leu Ser Asp Phe Arg Arg Glu Asn Glu Gly Tyr  
 203 100 105 110  
 206 Tyr Phe Cys Ser Ala Leu Ser Asn Ser Ile Met Tyr Phe Ser His Phe  
 207 115 120 125  
 210 Val Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg  
 211 130 135 140  
 214 Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg  
 215 145 150 155 160  
 218 Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Gly Asn Arg Arg Arg  
 219 165 170 175  
 222 Val Cys Lys Cys Pro Arg Pro Val Val Lys Ser Gly Asp Lys Pro Ser  
 223 180 185 190  
 226 Leu Ser Ala Arg Tyr Val  
 227 195

230 &lt;210&gt; SEQ ID NO: 4

231 &lt;211&gt; LENGTH: 2150

232 &lt;212&gt; TYPE: DNA

233 &lt;213&gt; ORGANISM: Homo sapiens

235 &lt;400&gt; SEQUENCE: 4

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 238 ccgcgcgcc tcccctcgcg ccgagcttc gagccaagca gcgtcctggg gagegcgtca 120  
 240 tggcettacc agtgaccgcc ttgtcctgc cgctggcctt gctgctccac gccgccaggc 180  
 242 cgagccagtt ccgggtgtcg ccgctggatc ggacctggaa cctgggcgag acagtggagc 240  
 244 tgaagtcca ggtgctgtcg tccaaccga cgtcgggctg ctggtggctc ttccagccgc 300  
 246 gcggcgccgc cgccagtccc accttctctc tatacctctc ccaaaacaag ccaaggcgg 360  
 248 ccgagggggt ggacaccag cggttctcgg gcaagagggt gggggacacc ttgctctca 420  
 250 ccctgagcga cttccgccga gagaacgagg gctactattt ctgctcggcc ctgagcaact 480  
 252 ccatcatgta cttcagccac ttctgtccgg tcttctctgc agcgaagccc accacgacgc 540  
 254 cagcgccgcg accaccaaca ccggcgccca ccatcgcgtc gcagcccctg tccctgcgcc 600  
 256 cagaggcgtg ccggccagcg gcggggggcg cagggaaccg aagacgtgtt tgcaaatgtc 660  
 258 cccggcctgt ggtcaaactg ggagacaagc ccagcctttc ggcgagatac gtctaaccct 720  
 260 gtgcaacagc cactacatta cttcaaactg agatccttcc ttttgaggga gcaagtccct 780  
 262 ccctttcatt ttttccagtc ttctccctg tgtattcatt ctcatgatta ttattttagt 840  
 264 gggggcgggg tgggaaagat tactttttct ttatgtgttt gacgggaaac aaaactaggt 900  
 266 aaaatctaca gtacaccaca agggtcacaa tactgttgtg cgcacatcgc ggtagggcgt 960

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268 ggaaaggggc aggccagagc taccgcgaga gttctcagaa tcatgctgag agagctggag 1020
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272 gagacagctt gatcaaaggc acacagcaag tcagggttgg agcagtagct ggagggacct 1140
274 tgtctcccag ctcagggtct tttcctccac accattcagg tctttctttc cgaggcccct 1200
276 gtctcagggt gaggtgcttg agtctccaac ggcaaggga caagtacttc ttgatacctg 1260
278 ggatactgtg cccagagcct cgaggaggta atgaattaaa gaagagaact gcctttggca 1320
280 gagttctata atgtaaaca tatcagactt ttttttttta taatcaagcc taaaattgta 1380
282 tagacctaaa ataaaatgaa gtggtgagct taacctgga aaatgaatcc ctctatctct 1440
284 aaagaaaatc tctgtgaaac ccctatgttg aggcggaatt gctctcccag cccttgcatt 1500
286 gcagaggggc ccatgaaaga ggacaggcta cccctttaca aatagaattt gagcatcagt 1560
288 gaggttaaac taaggccctc ttgaatctct gaatttgaga tacaacatg ttcctgggat 1620
290 cactgatgac tttttatact ttgtaaagac aattgttgga gagcccctca cacagccctg 1680
292 gcctctgctc aactagcaga tacagggatg aggcagacct gactctctta aggaggctga 1740
294 gagcccaaac tgctgtccca aacatgcact tccttgctta aggtatggtg caagcaatgc 1800
296 ctgcccattg gagagaaaaa acttaagtag ataaggaaat aagaaccact cataattctt 1860
298 caccttagga ataatctcct gttaatatgg tgtacattct tctgattat tttctacaca 1920
300 tacatgtaaa atatgtcttt cttttttaaa tagggttgta ctatgctgtt atgagtggct 1980
302 ttaatgaata aacatttgta gcctcctctt taatgggtaa acagcaaaaa aaaaaaaaaa 2040
304 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2100
306 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2150

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309 &lt;210&gt; SEQ ID NO: 5

310 &lt;211&gt; LENGTH: 198

311 &lt;212&gt; TYPE: PRT

312 &lt;213&gt; ORGANISM: Pongo pygmaeus

314 &lt;400&gt; SEQUENCE: 5

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316 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
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320 His Ala Ala Arg Pro Ser Gln Phe Arg Val Ser Pro Leu Asp Arg Thr
321 20 25 30
324 Trp Asn Leu Gly Glu Thr Val Glu Leu Lys Cys Gln Val Leu Leu Ser
325 35 40 45
328 Asn Pro Thr Ser Gly Cys Ser Trp Leu Phe Gln Pro Arg Gly Ala Ala
329 50 55 60
332 Ala Ser Pro Thr Phe Leu Leu Tyr Leu Ser Gln Asn Lys Pro Lys Ala
333 65 70 75 80
336 Ala Glu Gly Leu Asp Thr Gln Arg Phe Ser Gly Lys Arg Leu Gly Asp
337 85 90 95
340 Thr Phe Val Leu Thr Leu Ser Asp Phe Arg Arg Glu Asn Glu Gly Tyr
341 100 105 110
344 Tyr Phe Cys Ser Ala Leu Ser Asn Ser Ile Met Tyr Phe Ser His Phe
345 115 120 125
348 Val Pro Val Phe Leu Pro Val His Thr Arg Gly Leu Asp Phe Ala Cys
349 130 135 140
352 Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu
353 145 150 155 160
356 Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His Arg Asn Arg Arg Arg
357 165 170 175
360 Val Cys Lys Cys Pro Arg Pro Val Val Lys Ser Gly Gly Lys Pro Ser
361 180 185 190

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369 <211> LENGTH: 597
370 <212> TYPE: DNA
371 <213> ORGANISM: Pongo pygmaeus
373 <400> SEQUENCE: 6
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376 ccgagccagt tccgggtgtc gccctgggat cggacctgga acctgggcga gacggtggag      120
378 ctgaagtgcc aggtgctgct gtccaacccg acgtctggct gctcctggct cttccagccg      180
380 cgtggcgccg ccgccagtcc caccttcctc ctatacctct cccaaaacaa gccaaggcg      240
382 gccgaggggc tggacaccca gcggttctcg ggcaagaggt tgggggacac cttcgtcctc      300
384 accctgagcg acttcgcgcg ggagaacgaa ggctactatt tctgctcggc cctgagcaac      360
386 tccatcatgt acttcagcca cttegtgccg gtcttcctgc cagtgcacac gagggggctg      420
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396 <211> LENGTH: 310
397 <212> TYPE: PRT
398 <213> ORGANISM: Mus musculus
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407      20      25      30
410 Glu Leu Arg Ile Phe Pro Lys Lys Met Asp Ala Glu Leu Gly Gln Lys
411      35      40      45
414 Val Asp Leu Val Cys Glu Val Leu Gly Ser Val Ser Gln Gly Cys Ser
415      50      55      60
418 Trp Leu Phe Gln Asn Ser Ser Lys Leu Pro Gln Pro Thr Phe Val
419 65      70      75      80
422 Val Tyr Met Ala Ser Ser His Asn Lys Ile Thr Trp Asp Glu Lys Leu
423      85      90      95
426 Asn Ser Ser Lys Leu Phe Ser Ala Met Arg Asp Thr Asn Asn Lys Tyr
427      100     105     110
430 Val Leu Thr Leu Asn Lys Phe Ser Lys Glu Asn Glu Gly Tyr Tyr Phe
431      115     120     125
434 Cys Ser Val Ile Ser Asn Ser Val Met Tyr Phe Ser Ser Val Val Pro
435      130     135     140
438 Val Leu Gln Lys Val Asn Ser Thr Thr Thr Lys Pro Val Leu Arg Thr
439 145     150     155     160
442 Pro Ser Pro Val His Pro Thr Gly Thr Ser Gln Pro Gln Arg Pro Glu
443      165     170     175
446 Asp Cys Arg Pro Arg Gly Ser Val Lys Gly Thr Gly Leu Asp Phe Ala
447      180     185     190
450 Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Ile Cys Val Ala Leu
451      195     200     205
454 Leu Leu Ser Leu Ile Ile Thr Leu Ile Cys Tyr His Arg Ser Arg Lys

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**VERIFICATION SUMMARY**

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